

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Jessell, Thomas M.
Basler, Konrad
Yomada, Toshiya
- 10 (ii) TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
DORSALIN-1
- (iii) NUMBER OF SEQUENCES: 18
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham
(B) STREET: 30 Rockefeller Plaza
(C) CITY: New York
(D) STATE: New York
20 (E) COUNTRY: United States of America
(F) ZIP: 10112
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0576/40314
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40 (A) TELEPHONE: (212) 977-9550
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(C) TELEX: 422523 COOP UI
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1603 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 91..1371

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	CCTTTCCTCT	GTCTGTAAAG	ATTCAACATT	TTTAATCAGT	TAAAATACTT	TGTCCTCTTG	60
	TCTCTCCATC	AGAAAGTAAA	TACATAAGAA	ATG CAT TAT TTT	GGA GTA TTA GCT		114
				Met His Tyr Phe	Gly Val Leu Ala		
				1	5		
10	GCA CTG TCT GTT TTC AAT ATC ATT GCC TGC CTG ACA AGA GGC AAG CCT						162
	Ala Leu Ser Val Phe Asn Ile Ile Ala Cys Leu Thr Arg Gly Lys Pro						
	10		15		20		
15	TTG GAA AAC TGG AAA AAG CTA CCA GTT ATG GAA GAG TCT GAT GCA TTC						210
	Leu Glu Asn Trp Lys Lys Leu Pro Val Met Glu Glu Ser Asp Ala Phe						
	25		30		35		40
20	TTT CAT GAT CCT GGG GAA GTG GAA CAT GAC ACC CAC TTT GAC TTT AAA						258
	Phe His Asp Pro Gly Glu Val Glu His Asp Thr His Phe Asp Phe Lys						
		45		50		55	
25	TCT TTC TTG GAG AAT ATG AAG ACA GAT TTA CTA AGA AGT CTG AAT TTA						306
	Ser Phe Leu Glu Asn Met Lys Thr Asp Leu Leu Arg Ser Leu Asn Leu						
		60		65		70	
30	TCA AGG GTC CCC TCA CAA GTG AAG ACC AAA GAA GAG CCA CCA CAG TTC						354
	Ser Arg Val Pro Ser Gln Val Lys Thr Lys Glu Glu Pro Pro Gln Phe						
		75		80		85	
35	ATG ATT GAT TTA TAC AAC AGA TAT ACA GCG GAC AAG TCC TCC ATC CCT						402
	Met Ile Asp Leu Tyr Asn Arg Tyr Thr Ala Asp Lys Ser Ser Ile Pro						
		90		95		100	
40	GCA TCC AAC ATC GTG AGG AGC TTC AGC ACT GAA GAT GTT GTT TCT TTA						450
	Ala Ser Asn Ile Val Arg Ser Phe Ser Thr Glu Asp Val Val Ser Leu						
	105		110		115		120
45	ATT TCA CCA GAA GAA CAC TCA TTT CAG AAA CAC ATC TTG CTC TTC AAC						498
	Ile Ser Pro Glu Glu His Ser Phe Gln Lys His Ile Leu Leu Phe Asn						
		125		130		135	
50	ATC TCT ATT CCA CGA TAT GAG GAA GTC ACC AGA GCT GAA CTG AGA ATC						546
	Ile Ser Ile Pro Arg Tyr Glu Glu Val Thr Arg Ala Glu Leu Arg Ile						
		140		145		150	
55	TTT ATC TCC TGT CAC AAG GAA GTT GGG TCT CCC TCC AGA CTG GAA GGC						594
	Phe Ile Ser Cys His Lys Glu Val Gly Ser Pro Ser Arg Leu Glu Gly						
		155		160		165	
60	AAC ATG GTC ATT TAT GAT GTT CTA GAT GGA GAC CAT TGG GAA AAC AAA						642
	Asn Met Val Ile Tyr Asp Val Leu Asp Gly Asp His Trp Glu Asn Lys						
		170		175		180	
65	GAA AGT ACC AAA TCT TTA CTT GTC TCT CAC AGT ATT CAG GAC TGT GGC						690
	Glu Ser Thr Lys Ser Leu Leu Val Ser His Ser Ile Gln Asp Cys Gly						
	185		190		195		200
70	TGG GAG ATG TTT GAG GTG TCC AGC GCT GTG AAA AGA TGG GTC AAG GCA						738
	Trp Glu Met Phe Glu Val Ser Ser Ala Val Lys Arg Trp Val Lys Ala						
		205		210		215	
75	GAC AAG ATG AAG ACT AAA AAC AAG CTA GAG GTT GTT ATA GAG AGT AAG						786

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	Asp	Lys	Met	Lys	Thr	Lys	Asn	Lys	Leu	Glu	Val	Val	Ile	Glu	Ser	Lys	
				220					225					230			
5	GAT	CTG	AGT	GGT	TTT	CCT	TGT	GGG	AAG	CTG	GAT	ATT	ACT	GTT	ACT	CAT	834
	Asp	Leu	Ser	Gly	Phe	Pro	Cys	Gly	Lys	Leu	Asp	Ile	Thr	Val	Thr	His	
			235					240					245				
10	GAC	ACT	AAA	AAT	CTG	CCC	CTA	TTA	ATA	GTG	TTC	TCC	AAT	GAT	CGC	AGC	882
	Asp	Thr	Lys	Asn	Leu	Pro	Leu	Leu	Ile	Val	Phe	Ser	Asn	Asp	Arg	Ser	
		250					255					260					
15	AAT	GGG	ACA	AAA	GAG	ACC	AAA	GTG	GAG	CTC	CGG	GAG	ATG	ATT	GTT	CAT	930
	Asn	Gly	Thr	Lys	Glu	Thr	Lys	Val	Glu	Leu	Arg	Glu	Met	Ile	Val	His	
		265				270					275					280	
20	GAA	CAA	GAA	AGT	GTG	CTA	AAC	AAA	TTA	GGA	AAG	AAC	GAC	TCT	TCA	TCT	978
	Glu	Gln	Glu	Ser	Val	Leu	Asn	Lys	Leu	Gly	Lys	Asn	Asp	Ser	Ser	Ser	
					285					290					295		
25	GAA	GAA	GAA	CAG	AGA	GAA	GAA	AAA	GCC	ATT	GCT	AGG	CCC	CGT	CAG	CAT	1026
	Glu	Glu	Glu	Gln	Arg	Glu	Glu	Lys	Ala	Ile	Ala	Arg	Pro	Arg	Gln	His	
				300					305					310			
30	TCC	TCC	AGA	AGC	AAG	AGA	AGC	ATA	GGA	GCA	AAC	CAC	TGT	CGG	AGA	ACG	1074
	Ser	Ser	Arg	Ser	Lys	Arg	Ser	Ile	Gly	Ala	Asn	His	Cys	Arg	Arg	Thr	
			315					320					325				
35	TCA	CTC	CAT	GTG	AAC	TTT	AAA	GAA	ATA	GGT	TGG	GAT	TCT	TGG	ATC	ATT	1122
	Ser	Leu	His	Val	Asn	Phe	Lys	Glu	Ile	Gly	Trp	Asp	Ser	Trp	Ile	Ile	
		330					335					340					
40	GCA	CCC	AAA	GAT	TAT	GAG	GCT	TTT	GAG	TGT	AAA	GGA	GGT	TGC	TTC	TTC	1170
	Ala	Pro	Lys	Asp	Tyr	Glu	Ala	Phe	Glu	Cys	Lys	Gly	Gly	Cys	Phe	Phe	
		345				350					355				360		
45	CCC	CTC	ACA	GAT	AAT	GTT	ACG	CCA	ACC	AAA	CAT	GCT	ATT	GTC	CAG	ACT	1218
	Pro	Leu	Thr	Asp	Asn	Val	Thr	Pro	Thr	Lys	His	Ala	Ile	Val	Gln	Thr	
					365					370					375		
50	CTG	GTG	CAT	CTC	CAA	AAC	CCA	AAG	AAA	GCT	TCC	AAG	GCC	TGT	TGT	GTT	1266
	Leu	Val	His	Leu	Gln	Asn	Pro	Lys	Lys	Ala	Ser	Lys	Ala	Cys	Cys	Val	
				380				385						390			
55	CCA	ACT	AAA	TTG	GAT	GCA	ATC	TCT	ATT	CTT	TAT	AAG	GAT	GAT	GCT	GGT	1314
	Pro	Thr	Lys	Leu	Asp	Ala	Ile	Ser	Ile	Leu	Tyr	Lys	Asp	Asp	Ala	Gly	
			395					400					405				
60	GTG	CCC	ACT	TTG	ATA	TAT	AAC	TAT	GAA	GGG	ATG	AAA	GTG	GCA	GAA	TGT	1362
	Val	Pro	Thr	Leu	Ile	Tyr	Asn	Tyr	Glu	Gly	Met	Lys	Val	Ala	Glu	Cys	
		410					415					420					
65	GGC	TGC	AGG	TAGTATATGC	TGAATATCTA	AGAATATACT	CTTTTCTGCT										1411
	Gly	Cys	Arg														
		425															
70	GTCTGTGAAA	CTGTACATTA	GTGATGCAAA	TGAAAATCCT	TGCAAACAAG	GTTTGGAGCA											1471
75	CGGCATGGGG	CTGGTTGTTG	TTGCTGCTTT	TAAAGGAAAG	ATGGCATTTA	AAGAATGGCA											1531
80	ATCACTGTAA	ATACCCTGCA	TTATATACCA	TTAATTAAAA	CTTTGTGAGA	TTGAAAAAAA											1591
85	AAAAAAAAAA	AA															1603

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Tyr Phe Gly Val Leu Ala Ala Leu Ser Val Phe Asn Ile Ile
1 5 10 15
Ala Cys Leu Thr Arg Gly Lys Pro Leu Glu Asn Trp Lys Lys Leu Pro
20 25 30
Val Met Glu Glu Ser Asp Ala Phe Phe His Asp Pro Gly Glu Val Glu
35 40 45
His Asp Thr His Phe Asp Phe Lys Ser Phe Leu Glu Asn Met Lys Thr
50 55 60
Asp Leu Leu Arg Ser Leu Asn Leu Ser Arg Val Pro Ser Gln Val Lys
65 70 75 80
Thr Lys Glu Glu Pro Pro Gln Phe Met Ile Asp Leu Tyr Asn Arg Tyr
85 90 95
Thr Ala Asp Lys Ser Ser Ile Pro Ala Ser Asn Ile Val Arg Ser Phe
100 105 110
Ser Thr Glu Asp Val Val Ser Leu Ile Ser Pro Glu Glu His Ser Phe
115 120 125
Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg Tyr Glu Glu
130 135 140
Val Thr Arg Ala Glu Leu Arg Ile Phe Ile Ser Cys His Lys Glu Val
145 150 155 160
Gly Ser Pro Ser Arg Leu Glu Gly Asn Met Val Ile Tyr Asp Val Leu
165 170 175
Asp Gly Asp His Trp Glu Asn Lys Glu Ser Thr Lys Ser Leu Leu Val
180 185 190
Ser His Ser Ile Gln Asp Cys Gly Trp Glu Met Phe Glu Val Ser Ser
195 200 205
Ala Val Lys Arg Trp Val Lys Ala Asp Lys Met Lys Thr Lys Asn Lys
210 215 220
Leu Glu Val Val Ile Glu Ser Lys Asp Leu Ser Gly Phe Pro Cys Gly
225 230 235 240
Lys Leu Asp Ile Thr Val Thr His Asp Thr Lys Asn Leu Pro Leu Leu
245 250 255
Ile Val Phe Ser Asn Asp Arg Ser Asn Gly Thr Lys Glu Thr Lys Val
260 265 270

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Glu Leu Arg Glu Met Ile Val His Glu Gln Glu Ser Val Leu Asn Lys
 275 280 285
 5 Leu Gly Lys Asn Asp Ser Ser Ser Glu Glu Glu Gln Arg Glu Glu Lys
 290 295 300
 Ala Ile Ala Arg Pro Arg Gln His Ser Ser Arg Ser Lys Arg Ser Ile
 305 310 315 320
 10 Gly Ala Asn His Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu
 325 330 335
 Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe
 340 345 350
 15 Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro
 355 360 365
 Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys
 370 375 380
 Lys Ala Ser Lys Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser
 385 390 395 400
 25 Ile Leu Tyr Lys Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr
 405 410 415
 Glu Gly Met Lys Val Ala Glu Cys Gly Cys Arg
 420 425

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His
 1 5 10 15
 Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys
 20 25 30
 55 His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu
 35 40 45
 Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
 50 55 60
 60 Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu
 65 70 75 80

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Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val
85 90 95

Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu
100 105 110

Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val
115 120 125

Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Asp Gly Arg His Lys Ala Arg Ser Ile Arg Asp Val Ser Gly Gly
1 5 10 15

Glu Gly Gly Gly Lys Gly Gly Arg Asn Lys Arg His Ala Arg Arg Pro
20 25 30

Thr Arg Arg Lys Asn His Asp Asp Thr Cys Arg Arg His Ser Leu Tyr
35 40 45

Val Asp Phe Ser Asp Val Gly Trp Asp Asp Trp Ile Val Ala Pro Leu
50 55 60

Gly Tyr Asp Ala Tyr Tyr Cys His Gly Lys Cys Pro Phe Pro Leu Ala
65 70 75 80

Asp His Phe Asn Ser Thr Asn His Ala Val Val Gln Thr Leu Val Ala
85 90 95

Asn Asn Met Asn Pro Gly Lys Val Pro Lys Ala Cys Cys Val Pro Thr
100 105 110

Gln Leu Asp Ser Val Ala Met Leu Tyr Leu Asn Asp Gln Ser Thr Val
115 120 125

Val Leu Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys Gly Cys Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn
1 5 10 15
Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp
20 20 25 30
Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr
35 40 45
Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys
25 50 55 60
Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn
65 70 75 80
Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
30 85 90 95
Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys
35 100 105 110
Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile
115 120 125
Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
40 130 135 140

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
55 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

60 Glu Cys Lys Asp Ile Gln Thr Phe Leu Tyr Thr Ser Leu Leu Thr Val
1 5 10 15

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5 Thr Leu Asn Pro Leu Arg Cys Lys Arg Pro Arg Arg Lys Arg Ser Tyr
20 25 30

Ser Lys Leu Pro Phe Thr Ala Ser Asn Ile Cys Lys Lys Arg His Leu
35 40 45

10 Tyr Val Glu Phe Lys Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
50 55 60

Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu Cys Pro Tyr Pro Leu
65 70 75 80

15 Thr Glu Ile Leu Asn Gly Ser Asn His Ala Ile Leu Gln Thr Leu Val
85 90 95

His Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys Cys Val Pro Thr
100 105 110

20 Lys Met Ser Pro Ile Ser Met Leu Phe Tyr Asp Asn Asn Asp Asn Val
115 120 125

Val Leu Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys Gly Cys Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

45 Gly Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu
1 5 10 15

Gln Ala Arg Gln Ser Glu Asp His Pro His Arg Arg Arg Arg Gly
20 25 30

50 Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys Lys Lys Gln Phe Phe
35 40 45

Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp Ile Ile Ala Pro Ser
50 55 60

55 Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu Cys Pro Ser His Ile Ala
65 70 75 80

60 Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser Thr Val Ile Asn His
85 90 95

Tyr Arg Met Arg Gly His Ser Pro Phe Ala Asn Leu Lys Ser Cys Cys

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(2) INFORMATION FOR SEQ ID NO:8:

20 (ii) MOLECULE TYPE: protein

(111) HYPOTHETICAL: NO

(iv) ~~ANTI-SENSE~~: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

60 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Val Leu Glu Asp Ser Glu Thr Trp Asp Gln Ala Thr Gly Thr Lys
1 5 10 15
Thr Phe Leu Val Ser Gln Asp Ile Arg Asp Glu Gly Trp Glu Thr Leu
20 25 30
Glu Val Ser Ser Ala Val Lys Arg Trp Val Arg Ala Asp Ser Thr Thr
35 40 45
Asn Lys Asn Lys Leu Glu Val Thr Val Gln Ser His Arg Glu Ser Cys
50 55 60
Asp Thr Leu Asp Ile Ser Val Pro Pro Gly Ser Lys Asn Leu Pro Phe
65 70 75 80
Phe Val Val Phe Ser Asn Asp Arg Ser Asn Gly Thr Lys Glu Thr Arg
85 90 95
Leu Asp Leu Leu Lys Glu Met Ile Gly His Glu Gln Glu Thr Met Leu
100 105 110
Val Lys Thr Ala Lys Asn Ala Tyr Gln Gly Ala Gly Glu Ser Gln Glu
115 120 125
Glu Glu Gly Leu Asp Gly Tyr Thr Ala Val Gly Pro Leu Leu Ala Arg
130 135 140
Arg Lys Arg Ser Thr Gly Ala Ser Ser His Cys Gln Lys Thr Ser Leu
145 150 155 160
Arg Val Asn Phe Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro
165 170 175
Lys Glu Tyr Asp Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu
180 185 190
Ala Asp Asp Val Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val
195 200 205
His Leu Lys Phe Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr
210 215 220
Lys Leu Ser Pro Ile Ser Ile Leu Tyr Lys Asp Asp Met Gly Val Pro
225 230 235 240
Thr Leu Lys Tyr His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys
245 250 255
Arg

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(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGAATTCTG GVANGAYTGG ATHRTNGC

28

(2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGATCCAR NGTYTGNACD ATNGCRTG

28

(2) INFORMATION FOR SEQ ID NO:12:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGAATTCAT CGATAACGGA AGCTGAAGC

29

(2) INFORMATION FOR SEQ ID NO:13:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: YES

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10

AGCGTCGACA TCGATATTCA GCATATACTA CC

(2) INFORMATION FOR SEQ ID NO:14:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: YES

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAATTCGA TATCAGCTTC TGCTCTGCTC CTATGCTTCT CTTGC

45

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(2) INFORMATION FOR SEQ ID NO:15:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: YES

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGAATTCGA TATCCGAGGA GGACCTGAAC CACTGTCGGA GAACGTC

47

(2) INFORMATION FOR SEQ ID NO:16:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ile Gly Ala Glu Gln Lys Leu Ile Ser

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(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:17:

20

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(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

35

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

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